

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: June 23, 2003, 08:28:51 ; Search time 20.5204 Seconds

(without alignments)
371.904 Million cell updates/sec

Title: US-10-077-137-1

Perfect score: 964
Sequence: 1 MLOWAGCCSNEYFDLHA.....CKSLPALATEIKSISAR 184

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

al number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	964	100.0	184	TR17 HUMAN	Q02223 homo sapien
2	572	59.3	185	TR17 MOUSE	O08472 mus musculi
3	116.5	12.1	175	TI13C MOUSE	Q9d6d0 mus musculi
4	94	9.8	323	TNR6 BOVIN	P51867 bos taurus
5	93	9.6	184	TI13C HUMAN	Q96c13 homo sapien
6	86.5	9.0	867	PROM MOUSE	O54930 mus musculi
7	82	8.5	1009	PAK2 MOUSE	Q99p99 mus musculi
8	82	8.5	1009	PAK2 RAT	P70600 rattus norv
9	79.5	8.2	1009	PAK2 HUMAN	Q14289 h protein t
10	78.5	8.1	293	TI13X HUMAN	O14836 homo sapien
11	78.5	8.1	249	TI13X MOUSE	O58752 methanococ
12	77	8.0	249	TI13X MOUSE	Q9e435 mus musculi
13	75.5	7.8	638	YCSB SCHPO	O07490 schizosacch
14	75	7.8	849	SRK6 BRAOL	Q09092 brisella o1
15	74.5	7.7	384	ERD1 KULIA	P41771 kluyveromyc
16	72.5	7.5	1013	PRML DROME	P82295 drosophila
17	71.5	7.4	105	Y078 NPVOP	O10331 oxygia pseu
18	71.5	7.4	627	Y017 RICPR	Q92ec6 rickettsia
19	71	7.4	227	COMB THEMA	Q9wq44 thermotoga
20	70.5	7.3	188	Y101 UREPA	Q9p143 ureaplasma
21	70.5	7.3	1203	MGR5 RAT	P31224 rattus norv
22	70.5	7.3	1877	PCK5 MOUSE	O04592 mus musculi
23	70.5	7.3	2715	G156 PARPR	P13837 paramectum
24	70	7.3	654	HS70 TRIRU	O93866 trichophyto
25	69.5	7.2	573	TLPC_BACSU	P39209 bacillus su
26	69.5	7.2	1212	MGR5 HUMAN	P41594 homo sapien
27	69.5	7.2	5376	ZAN MOUSE	O08799 mus musculi
28	69	7.2	324	GCI MOUSE	P01868 mus musculi
29	69	7.2	352	CSAE RAT	P97520 rattus norv
30	69	7.2	379	PANE YEAST	P38787 saccharomyc
31	69	7.2	393	GC1A MOUSE	P01869 mus musculi
32	69	7.2	416	R23B MOUSE	P54728 mus musculi
33	68.5	7.1	321	O5V1_HUMAN	Q9ugf6 homo sapien

34	68.5	7.1	328	1	Y679 CHILMU	Q9pj27 chlamydia m
35	68.5	7.1	409	1	R23B HUMAN	P54727 homo sapien
36	68.5	7.1	575	1	C662 CUUMA	O05046 cucurbita m
37	68.5	7.1	576	1	C662 MAIZE	O43298 zea mays (m
38	68.5	7.1	577	1	C661 MAIZE	P23185 zea mays (m
39	68	7.1	590	1	ACCD_PEA	P18823 pisum sativ
40	68	7.1	1140	1	RA18 SCHPO	P53692 schizosacch
41	68	7.1	1203	1	XCPE XENLA	P50533 xenopus lae
42	68	7.1	2158	1	MY9B HUMAN	O13459 homo sapien
43	68	7.1	3386	1	POLG_DEN4	P09866 d genome po
44	67.5	7.0	178	1	LACB_BOVIN	P02754 bos taurus
45	67.5	7.0	245	1	YH77_ARCFU	O28497 archaeglob

ALIGNMENTS

RESULT 1	ID	TR17 HUMAN	STANDARD;	PRT;	184 AA.
AC	Q02223;				
DT	01-JUL-1993 (Rel. 26, Last sequence update)				
DT	01-JUL-1993 (Rel. 26, Last sequence update)				
DT	15-JUN-2002 (Rel. 41, Last annotation update)				
DE	Tumor necrosis factor receptor superfamily member 17 (B-cell maturation protein).				
GN	TNFRSF17 OR BCMA OR BCM.				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.				
OX	NCBI_TaxID=9606;				
OX	[1]				
RP	SEQUENCE FROM N.A., AND CHROMOSOMAL TRANSLOCATION.				
RC	TISSUE=Peripheral blood leukocytes, and lymph node.				
RX	MEDLINE=93010984; PubMed=1396583;				
RA	Laabi Y., Gras M.P., Cardonnel F., Brouet J.C., Berger R., Larsen C.J., Tsapis A.;				
RA	Laabi Y., Gras M.P., Cardonnel F., Brouet J.C., Berger R., Larsen C.J., Tsapis A.;				
RT	"A new gene, BCM, on chromosome 16 is fused to the interleukin 2 gene by a t(4;16)(q26;p13) translocation in a malignant T cell lymphoma.";				
RT	EMBO J. 11:3897-3904(1992).				
RL	[2]				
RN	SEQUENCE FROM N.A.				
RP	MEDLINE=94218235; PubMed=8165126;				
RX	Laabi Y., Gras M.P., Brouet J.C., Berger R., Larsen C.J., Tsapis A.;				
RA	Fuhrman U., Mason T., Crosby M.L., Barnstead M., Cronin L., Deslattes Mays A., Cao Y., Xu R.X., Kang H.-L., Mitchell S., Eichler E.E., Harris P.C., Venter J.C., Adams M.D.;				
RA	"Genome duplications and other features in 12 Mb of DNA sequence from human chromosome 16p and 16q.";				
RT	Genomics 60:295-308(1999).				
RL	[3]				
RN	SEQUENCE FROM N.A.				
RP	MEDLINE=9425270; PubMed=10493829;				
RX	Loftus B.J., Kim U.-J., Sneddon V.P., Kalush F., Brandon R., Fuhrman U., Mason T., Crosby M.L., Barnstead M., Cronin L., Deslattes Mays A., Cao Y., Xu R.X., Kang H.-L., Mitchell S., Eichler E.E., Harris P.C., Venter J.C., Adams M.D.;				
RA	"Presence of four major haplotypes in human BCMA gene: lack of association with systemic lupus erythematosus and rheumatoid arthritis.";				
RT	Genes Immun. 2:276-279(2001).				
RL	[4]				
RN	SEQUENCE FROM N.A., AND VARIANT THR-153.				
RP	MEDLINE=21419161; PubMed=11528522;				
RX	Kawasaki A., Tsuchiya N., Fukazawa T., Hashimoto H., Tokunaga K.;				
RA	"Presence of four major haplotypes in human BCMA gene: lack of association with systemic lupus erythematosus and rheumatoid arthritis.";				
RT	Genes Immun. 2:276-279(2001).				
RL	[5]				
RN	FUNCTION.				
RP	MEDLINE=2036316; PubMed=10903733;				
RX	Hatzoglou A., Roussel J., Bourgade M.-F., Rogier E., Madry C., Inoue J., Devergne O., Tsapis A.;				
RA	"TNF receptor family member BCMA (B cell maturation) associates with TNF receptor-associated factor (TRAF) 1, TRAF2, and TRAF3 and activates NF-kappa B, elk-1, c-Jun N-terminal kinase, and p38				

RT mitogen-activated protein kinase.";
 RL J. Immunol. 165:1332-1330(2000).
 [6]
 RP FUNCTION
 RA MEDLINE=20259066; PubMed=10801128;
 RX Gross J.A., Johnston J., Mudri S., Enselman R., Dillon S.R.,
 RA Madden K., Xu W., Parish-Novak J., Foster D., Lofton-Day C.,
 RA Moore M., Litteu A., Grossman A., Haugen H., Foley K., Blumberg H.,
 RA Harrison K., Kindvogel W., Clegg C.H.;
 RT "TAC1 and BCMA are receptors for a TNF homologue implicated in B-cell
 auto-immune disease.";
 RL Nature 404:995-999(2000).
 [7]
 RP FUNCTION, AND INTERACTION WITH APRIL AND BAFF.
 RX MEDLINE=2110294; PubMed=10973284;
 RA Yu G., Boone T., Delaney J., Hawkins N., Kelley M., Ramakrishnan M.,
 RA McCabe S., Qiu W.R., Kornuc M., Xia X.-Z., Guo J., Stolina M.,
 RA Boyle W.J., Sarosi I., Hsu H., Senaldi G., Theil L.E.;
 RT "APRIL and TALL-1 and receptors BCMA and TAC1: system for regulating
 humoral immunity.";
 RL Nat. Immunol. 1:252-256(2000).
 [8]
 RP INTERACTION WITH TRAF5 AND TRAF6.
 RX MEDLINE=20381353; PubMed=10908663;
 RA Shu H.-B., Johnson H.;
 RT "B cell maturation protein is a receptor for the tumor necrosis factor
 family member TALL-1.";
 RL Proc. Natl. Acad. Sci. U.S.A. 97:9156-9161(2000).
 CC -1- FUNCTION: Receptor for TNFSF13B/BLyS/BAFF and TNFSF13/APRIL.
 CC Promotes B-cell survival and plays a role in the regulation of
 CC humoral immunity. Activates NF-kappa-B and JNK.
 CC -1- SUBUNIT: Associates with TRAF1, TRAF2, TRAF3, TRAF5 and TRAF6.
 CC -1- SUBCELLULAR LOCATION: Type III membrane protein. Plasma membrane
 CC and perinuclear Golgi-like structures.
 CC -1- TISSUE SPECIFICITY: Expressed in mature B-cells, but not in T-
 CC cells or monocytes.
 CC -1- DISEASE: A FORM OF T-CELL ACUTE LYMPHOBLASTIC LEUKEMIA (T-ALL) IS
 CC CHARACTERIZED BY A CHROMOSOMAL TRANSLOCATION T(4;16)(Q26;P13)
 CC WHICH INVOLVES BCMA AND IL2.
 CC -1- SIMILARITY: CONTAINS 1 TNFR-CYS REPEAT.
 CC -----
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 CC -----
 DR EMBL; Z14954; CAAT7679.1; -;
 DR EMBL; Z29575; CAAB2691.1; -;
 DR EMBL; Z29574; CAAB2690.1; -;
 DR EMBL; U95742; AAB67251.1; -;
 DR EMBL; AB052772; BAB60895.1; -;
 DR PIR; S31208; S31208.
 DR PIR; S31209; S31209.
 DR Genem; HGNC:11913; TNFRSF17.
 DR MIM; 109545; -;
 KW Receptor; Immune response; Proto-oncogene; Signal-anchor;
 KW Transmembrane; Chromosomal translocation; Polymorphism.
 KW DOMAIN 1 54
 KW TRANSMEM 55 77
 KW SIGNAL-ANCHOR (TYPE III MEMBRANE PROTEIN)
 KW (POTENTIAL)
 KW CYTOPLASMIC (POTENTIAL).
 KW TNFR-CYS.
 KW BREAKPOINT FOR TRANSLOCATION TO FORM
 KW INTERLEUKIN 2/BCM ONCOGENE.
 KW DISUPEID 8 21
 KW DISUPEID 24 37
 KW DISUPEID 26 41
 KW VARIANT 153 153
 KW A -> T.
 KW /FTID=VAR_012234.
 KW SEQUENCE 184 AA; 20138 MW; 277AF11E2767D932 CRC64;

Query Match 100.0%; Score 964; DB 1; Length 184;
 Best Local Similarity 100.0%; Pred. No. 1,3e-83;
 Matches 184; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MWMAGGCGSNGYFDSLLHACIPQLRCSSNTPPLTCRCYCNASVTNSVKGTAIWLTC 60
 DB 1 MWMAGGCGSNGYFDSLLHACIPQLRCSSNTPPLTCRCYCNASVTNSVKGTAIWLTC 60
 QY 61 GSIILSLAVFLMFLKRISEPKDKFKNKSGSLGMANDLKSRTGDEILIPRGE 120
 DB 61 GSIILSLAVFLMFLKRISEPKDKFKNKSGSLGMANDLKSRTGDEILIPRGE 120
 QY 121 YVSECTCEDCKSKPKYSDHCPPLPMMEGATLVTTKNDYCKSLPALSAITEIKS 180
 DB 121 YVSECTCEDCKSKPKYSDHCPPLPMMEGATLVTTKNDYCKSLPALSAITEIKS 180
 QY 181 ISAR 184
 DB 181 ISAR 184
 RESULT 2
 ID TR17 MOUSE STANDARD; PRI; 185 AA.
 AC 088472;
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 17 (B-cell
 DE maturation protein).
 GN TNFSF17 OR BCMA OR BCM.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1 AND 2).
 RC STRAIN=BALB/C; TISSUE=Spleen;
 RX MEDLINE=99061155; PubMed=9846698;
 RA Madry C., Laabi Y., Callebaut I., Rousset J., Hatzoglou A.,
 RA Le Condat M., Morron J.P., Berger R., Tsapis A.;
 RT "The characterization of murine BCMA gene defines it as a new member
 RL of the tumor necrosis factor receptor superfamily.";
 RL Int. Immunol. 10:1693-1702(1998).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC STRAIN=C57BL/6J; TISSUE=Colon;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai T., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Cavalet T.,
 RA Pleischmann W., Gaasterland T., Gissi C., King B., Kochia H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.W., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Hono H., Balderelli R., Barsh G.,
 RA Blake J., Botfield D., Boujunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., But C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzaletti J., Mombereaux P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Sessa T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyokawa K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Haegawa Y., Kawaji H., Kohlschut S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 CC -1- FUNCTION: Receptor for TNFSF13B/BLyS/BAFF and TNFSF13/APRIL.
 CC Promotes B-cell survival and plays a role in the regulation of
 CC humoral immunity. Activates NF-kappa-B and JNK (By similarity).
 CC -1- SUBUNIT: Associates with TRAF1, TRAF2, TRAF3, TRAF5 and TRAF6 (By

```

CC      similarity).
CC      -1- SUBCELLULAR LOCATION: Type III membrane protein (Probable).
CC      -1- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; are
CC      produced by alternative splicing.
CC      -1- TISSUE SPECIFICITY: Detected in spleen, thymus, bone marrow and
CC      heart, and at lower levels in kidney and lung.
CC      -1- SIMILARITY: CONTAINS 1 TNFR-CYS REPEAT.
CC      -----
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CC      -----
CC      EMBL: AF061505; AAC23799.1; -.
CC      EMBL: AK020247; BAB32038.1; -.
CC      MGD: MGI:1343050; Tnfrsf17.
CC      Receptor; Immune response; Signal-anchor; Transmembrane;
CC      Alternative splicing.
CC      DOMAIN
CC      TRANSMEM 1 49 EXTRACELLULAR (POTENTIAL)
CC      SIGNAL-ANCHOR (TYPE III MEMBRANE PROTEIN)
CC      (POTENTIAL).
CC      CYTOPLASMIC (POTENTIAL).
CC      REPEAT 4 185
CC      TNFR-CYS.
CC      BY SIMILARITY.
CC      DISULFID 5 18
CC      BY SIMILARITY.
CC      DISULFID 21 32
CC      BY SIMILARITY.
CC      FT DISULFID 25 36
CC      VARSPLIC 87 91 MISSING (IN ISOFORM 2).
CC      SQ SEQUENCE 185 AA; 20442 MW; 8806352B4FD26A8E CRC64;
CC
CC      Query Match 59.3%; Score 572; DB 1; Length 185;
CC      Best Local Similarity 62.6%; Pred. No. 8,7e-47;
CC      Matches 117; Conservative 21; Mismatches 41; Indels 8; Gaps 4;
CC
QY      4 MAGQSQNVEFDSLHACIPCOLRCSNTPPTQCRYYCNASYNSYKGNATLMTCLGIS 63
DB      1 MAQCFHSEYFDSLHACKRCHLRGNN--PPATCQYCDPSTVSSKGYTVMFLGLT 58
QY      64 LIISLAVFLMLKRISEPLKDEPKA---TSGGLGMANIDLEKSTGDEIILPRGL 119
DB      59 IVLISLALFTISFLKRMPEAKDEPOSGQLDGSNQLDKADTELRIKAGDRIFFPRSL 118
QY      120 EYTVECTCECDCKSKPKYVDSHCPFLPMERGAATLVTTKNDYCK-SLPAAL-SATFI 177
DB      119 EYTVECTCECDCKSKPKGSDHFFPLPMERGAATLVTTKTDYKSSVPTALOSVWGM 178
QY      178 EKSIASR 184
DB      179 EKPTHTR 185
CC
DB      179 EKPTHTR 185
CC
CC      RESULT 3
CC      T13C MOUSE STANDARD; PRT; 175 AA.
CC      ID T13C MOUSE
CC      AC Q9D8D0;
CC      DT 15-JUN-2002 (Rel. 41, Last sequence update)
CC      DT 15-JUN-2002 (Rel. 41, Last annotation update)
CC      DE Tumor necrosis factor receptor superfamily member 13C (B cell-
CC      activating factor receptor) (BAFF receptor) (BAFF-R) (Blys receptor
CC      3) (B-cell maturation defect).
CC      DE TNPSP13C OR BAFFR OR BCMd OR BR3.
CC      OS Mus musculus (Mouse).
CC      OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC      OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CC      NCBI_TaxID=10090;
CC      NP NCBI
CC      RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
CC      RC STRAIN=BALE/c; TISSUE=B-cell lymphoma;
CC      RX MEDLINE=21442025; PubMed=11509592;
CC      Thompson J.S., Bixler S.A., Qian F., Vora K., Scott M.L.,

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RA      Cachero T.G., Hession C., Schneider P., Sizing I.D., Mullen C.,
RA      Struch K., Zafari M., Benjamin C.D., Teichopp J., Browning J.L.,
RA      Ambrose C.;
RA      "BAFF-R, a newly identified TNF receptor that specifically interacts
RA      with BAFF.";
RA      Science 293:2108-2111 (2001).
RA      [2]
RA      SEQUENCE FROM N.A. (ISOFORM 1), AND DISEASE.
RA      RP STRAIN=A/J;
RA      RC MEDLINE=21475520; PubMed=11591325;
RA      RX Yan M., Brady J.R., Chan B., Lee W.P., Hsu B., Harless S.M.,
RA      Canoro M.P., Grewal I.S., Dixit V.M.;
RA      "Identification of a novel receptor for B lymphocyte stimulator that
RA      is mutated in a mouse strain with severe B cell deficiency.";
RA      Curr. Biol. 11:1547-1552 (2001).
RA      [3]
RA      SEQUENCE FROM N.A. (ISOFORM 1),
RA      RC STRAIN=C57BL/6J; TISSUE=Small intestine;
RA      RX MEDLINE=21085660; PubMed=11217851;
RA      Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA      Aizawa K., Izawa M., Niehi K., Kiyosawa H., Kondo S., Yamataka I.,
RA      Satoh T., Okazaki Y., Gojodori T., Bono H., Kasukawa T., Saito R.,
RA      Kadoya K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA      Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA      Kuehl P., Lewis S., Matano Y., Nikaido I., Pesole G., Quackenbush J.,
RA      Schriml L.M., Stuhli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA      Sakai K., Okino T., Furuno M., Kono H., Baldarelli R., Barsh G.,
RA      Blake J., Botfeill D., Boujunga N., Carninci P., de Bonaldo M.F.,
RA      Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,
RA      Guestinich S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,
RA      Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA      Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA      Saeki H., Sato K., Schenbach C., Seya T., Shibata Y., Storch K.-F.,
RA      Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA      Wymshak-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohlsaki S.,
RA      Hayashizaki Y.;
RA      "Functional annotation of a full-length mouse cDNA collection.";
RA      Nature 409:685-690 (2001).
RA      [4]
RA      FUNCTION.
RA      RP MEDLINE=21614654; PubMed=11747827;
RA      RX Harless S.M., Lentz V.M., Sah A.P., Hsu B.L., Clise-Dwyer K.,
RA      Hilbert D.M., Hayes C.E., Canoro M.P.;
RA      "Competition for Blys-mediated signaling through BcmD/BR3 regulates
RA      peripheral B lymphocyte numbers.";
RA      Curr. Biol. 11:1986-1989 (2001).
RA      [1]
RA      FUNCTION: B-cell receptor specific for TNFSF13B/TALL1/BAFF/Blys.
RA      Promotes the survival of mature B-cells and the B-cell response.
RA      -1- SUBCELLULAR LOCATION: Type III membrane protein (Probable).
RA      -1- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; are
RA      produced by alternative splicing.
RA      -1- TISSUE SPECIFICITY: Highly expressed in spleen and testis;
RA      detected at lower levels in lung and thymus.
RA      -1- DISEASE: Defects in TNFSF13C are a cause of severe B-cell
RA      deficiency. B-cell deficient strain A/WShu has a 4.7 kb insertion
RA      in the BAFFR gene leading to an altered C-terminus. The mutant RNA
RA      is not detectable. B-cell lymphoplasia is normal, but the life
RA      span of peripheral B-cells is much reduced.
RA      -1- SIMILARITY: CONTAINS 1 TNFR-CYS REPEAT.
RA      -----
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RA      -----
RA      EMBL: AF373847; AAK91827.1; -.
RA      EMBL: AK008142; BAB25490.1; -.
RA      MGD: MGI:1919299; Tnfrsf13c.
RA      Receptor; Immune response; Signal-anchor; Transmembrane; Glycoprotein;

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Alternative splicing.
 KM DOMAIN 1 71 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 72 92 SIGNAL-ANCHOR (TYPE III MEMBRANE PROTEIN)
 FT (POTENTIAL).
 FT DOMAIN 93 175 CYTOPLASMIC (POTENTIAL).
 FT REPEAT 21 38 TNFR-CYS (PARTIAL).
 FT DISULFID 22 35 BY SIMILARITY.
 FT DISULFID 27 36 BY SIMILARITY.
 FT CARBOHYD 23 23 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT VARSPLIC 133 143 MISSING (IN ISOCOREM 2).
 SQ SEQUENCE 175 AA; 18798 MW; 28BC7C1A02PB87EP CRC64;
 Query Match 12.1%; Score 116.5; DB 1; Length 175;
 Best Local Similarity 29.4%; Pred. No. 0.00051;
 Matches 50; Conservative 21; Mismatches 64; Indels 35; Gaps 8;
 QY 7 QCSQNEYPFSLHACIPCOL-----RCSSNTPPLTCQRYCNASTNSYK--GNNAIL 56
 DB 21 QCNQTECFDPLVNCVSCCLFHTPTGHTSSLEPGTALPQEGSALRPVALLVGPALL 80
 57 WTCLGLSLI--ISLAFVLMFLRKIS---SEBLKDFKNTSGGLGMANIDKSRGTD 111
 DB 81 GLIILALTLVGLVSLVSMRMRQQLRTASPTDSGVQGE-----SLENVFPSSSET-- 129
 QY 112 EILIPRGLEYTVECTCECDIKSKPKVSDHCFPLPAMEBGATILVTTKT 161
 DB 130 ----PHASAPTWPEPLK-EDADSALPR-----HSPVPRATLSTGLVLTTKT 170
 RESULT 4
 ID TNFR6 BOVIN STANDARD; PRT; 323 AA.
 AC P51867;
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-1996 (Rel. 41, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 6 precursor (FASL receptor) (Apoptosis-mediating surface antigen FAS) (Apo-1 antigen) (CD95).
 DE (CD95).
 GN TNFRSF6 OR APT1 OR FAS.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bovine; Bos.
 OC NCB1_Taxid=9913;
 RX (1)
 RP SEQUENCE FROM N.A.
 MEDLINE=96226401; PubMed=8634151;
 Yoo J., Stone R.T., Beattie C.W.;
 "Cloning and characterization of the bovine Fas.",
 DNA Cell Biol. 15:227-234(1996).
 CC -1- FUNCTION: Receptor for TNFRSF6/FASL. The adaptor molecule FADD recruits caspase-8 to the activated receptor. The resulting death-inducing signaling complex (DISC) performs caspase-8 proteolytic activation which initiates the subsequent cascade of caspases (aspartate-specific cysteine proteases) mediating apoptosis. FAS-mediated apoptosis may have a role in the induction of peripheral tolerance, in the antigen-stimulated suicide of mature T-cells, or both (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD, AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.
 CC -1- SIMILARITY: CONTAINS 3 TNFR-CYS REPEATS.
 CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
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 CC

DR EMBL; U34794; AAC48546.1; -.
 DR HSSP; P25445; 1DDF.
 DR InterPro; IPR000488; Death.
 DR InterPro; IPR001368; TNFR_C6.
 DR Pfam; PF00020; TNFR_C6; 3.
 DR Pfam; PF00531; death; 1.
 DR SMART; SM00208; TNFR; 3.
 DR SMART; SM00205; DEATH; 1.
 DR PROSITE; PS00652; TNFR_NGFR_1; 2.
 DR PROSITE; PS00652; TNFR_NGFR_2; 2.
 DR PROSITE; PS50017; DEATH_DOMAIN; 1.
 DR PROSITE; PS50017; DEATH_DOMAIN; 1.
 KW Receptor; Apoptosis; Glycoprotein; Transmembrane; Repeat; Signal.
 FT SIGNAL 1 16 POTENTIAL.
 FT CHAIN 17 323 TUMOR NECROSIS FACTOR RECEPTOR
 FT TRANSMEM 17 170 SUPERFAMILY MEMBER 6.
 FT DOMAIN 171 188 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 189 323 POTENTIAL.
 FT REPEAT 45 80 CYTOPLASMIC (POTENTIAL).
 FT REPEAT 81 124 TNFR-CYS 1.
 FT REPEAT 125 163 TNFR-CYS 2.
 FT REPEAT 238 306 TNFR-CYS 3.
 FT DOMAIN 45 56 DEATH.
 FT DISULFID 57 70 BY SIMILARITY.
 FT DISULFID 60 79 BY SIMILARITY.
 FT DISULFID 82 98 BY SIMILARITY.
 FT DISULFID 101 116 BY SIMILARITY.
 FT DISULFID 124 124 BY SIMILARITY.
 FT DISULFID 126 140 BY SIMILARITY.
 FT DISULFID 143 154 BY SIMILARITY.
 FT DISULFID 146 162 BY SIMILARITY.
 FT CARBOHYD 38 38 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 115 115 N-LINKED (GLCNAC. .) (POTENTIAL).
 SQ SEQUENCE 323 AA; 36445 MW; 4D88A903E9E1F4892 CRC64;
 Query Match 9.8%; Score 94; DB 1; Length 323;
 Best Local Similarity 22.1%; Pred. No. 0.13;
 Matches 51; Conservative 33; Mismatches 65; Indels 82; Gaps 15;
 QY 8 CSQ-NEYRPSDLHA--CIPCOL-----RCSSN-----T 32
 DB 82 CSEGEHYTDKSHSHSCIRCSICDEHGLEVBQNTTRNTKCKSNPFCNSPCEHCN 141
 QY 33 PPLTCQ----RYCNASTNSYKTVNA--IIMTCLGLSLISLAFVLMFLRKISSEPL 85
 DB 142 PCTTCEHGLEIEKCTPTSNMTKCGSHANSJMAL-----LILLIPVLIIYKVVSREBNK 197
 QY 86 KQEFKNTSGG-----LIGMANIDL-----EKSRGTD--EILIPRGLEYTVECTCED 130
 DB 198 KNDYCNSAASNDGRLMLTDVLDGKYTPSIAEQWRITEVEFEYKQNM---BEAKTID 253
 QY 131 CIKSKPKVSDHCFPLPAMEBGATILV-----TKTNDYC--KSLPAALS 173
 DB 254 IWH-----DNVA---ETAEQKVQLRWYQSHGKNAYCTLTSLPPLA 295
 RESULT 5
 ID T13C HUMAN STANDARD; PRT; 184 AA.
 AC Q96R03;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 13C (B cell-activating factor receptor) (BAFF receptor) (BAFF-R) (Blys receptor 3).
 GN TNFRSF13C OR BAFFR OR BR3.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OC NCB1_Taxid=9606;
 RX (1)
 RP SEQUENCE FROM N.A. (ISOCOREM 1 AND 2).
 CC

RTISUB-B-cell lymphoma;
 RX MEDLINE=21442025; PubMed=11509692;
 RA Thompson J.S., Bixler S.A., Qian F., Vora K., Scott M.L.,
 RA Cachero T.G., Hession C., Schneider P., Sizing I.D., Mullen C.,
 RA Struch K., Zafar M., Benjamin C.D., Tschopp J., Browning J.L.,
 RA Ambrose C.;
 RA "BAF-R, a newly identified TNF receptor that specifically interacts
 RT with BAF-R";
 RL Science 293:2108-2111 (2001).

RP [2]

FUNCTION.

RX MEDLINE=21475520; PubMed=11591325;
 RA Van M., Brady J.R., Chan B., Lee W.P., Hau B., Harless S.M.,

RA Canero M.P., Grewal I.S., Dixit V.M.;

RT "Identification of a novel receptor for B lymphocyte stimulator that
 RL is mutated in a mouse strain with severe B cell deficiency.";

RL Curr. Biol. 11:1547-1552 (2001).

CC -1- FUNCTION: B-cell receptor specific for TNFSF13B/TALL1/BAFF/BLYS.
 CC Promotes the survival of mature B-cells and the B-cell response.

CC -1- SUBCELLULAR LOCATION: Type III membrane protein (Probable).

CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; may be
 CC produced by alternative splicing.

CC -1- TISSUE SPECIFICITY: Highly expressed in spleen and lymph node, and
 CC in resting B-cells. Detected at lower levels in activated B-cells,
 CC resting CD4+ T-cells, in thymus and peripheral blood leukocytes.

CC -1- SIMILARITY: CONTAINS 1 TNFR-CYS REPEAT.

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CC EMBL; AF373846; AAK91826.1; -

DR Genew; HGNC:17755; TNFRSF13C.

DR MIM; 606269; -

DR PROSITE; PS00652; TNFR_NGFR_1; FALSE_NEG.

KW PROSITE; PS50050; TNFR_NGFR_2; FALSE_NEG.

KW Receptor; Immune response; Signal-anchor; Transmembrane;

KW Alternative splicing.

CC DOMAIN 1 78 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 79 99 SIGNAL-ANCHOR (TYPE III MEMBRANE PROTEIN)

FT DOMAIN 100 184 CYTOPLASMIC (POTENTIAL).

FT REPEAT 18 35 TNFR-CYS (PARTIAL).

FT DISULFID 19 32 BY SIMILARITY.

FT DISULFID 24 35 BY SIMILARITY.

FT VARSPLIC 143 143 P -> PA (IN ISORFORM 2).

CC SEQUENCE 184 AA, 18863 MW; F2BFB9809A27138 CR664;

Query Match 9.6%; Score 93; DB 1; Length 184;

Best Local Similarity 26.5%; Pred. No. 0.088;

Matches 48; Conservative 20; Mismatches 65; Indels 48; Gaps 8;

QY 8 CSQNYEFDLHACIPCOQ-----RCSSNTP--PLTCQRYCASTNSVKGKNAI 56

DB 19 CVPACSCFDLVHRCVACGLRTPPKAGASSPAPPTALQPOESVAGAGEALPLPGIL 78

QY 57 W---TCLGSLIISLAVFLMF-----LTKRISSEPLKDEPNTGSGILGMANIDLEKS 107

DB 79 FAPALLGLALVIALVGLVSMRRQRRLRGASSAEADGKDAPEL----- 127

QY 108 RTGDEIILPRGLELYVEECTC-----EDCIKSKPKVDSDHCPLPAMEGATILVTTK 160

DB 128 ---DKVYI---LSPGISDATALPAMPPEPPTTP-----GASVVPATLSTELVTTK 177

QY 161 T 161

DB 178 T 178

RESULT 6
 ID PROM MOUSE STANDARD; PRT; 867 AA.

AC 054930; 035408; 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Prominin precursor (Antigen AC133 homolog).

GN PROM.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

OX NCBI_Taxid=10090;

RP [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Brain;

RA Mitzigila S., Godfrey W., Buck D.;

RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.

RP [2]

RP SEQUENCE FROM N.A.

RC TISSUE=Kidney;

RX MEDLINE=98024147; PubMed=9356465;

RA Weigmann A., Corbell D., Hellwig A., Huttner W.B.;

RT "Prominin, a novel microvilli-specific polytopic membrane protein of
 RT the apical surface of epithelial cells, is targeted to plasmalemma

RT protrusions of non-epithelial cells.";

RL Proc. Natl. Acad. Sci. U.S.A. 94:12425-12430 (1997).

CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).

CC -1- TISSUE SPECIFICITY: IN THE EMBRYO, EXPRESSED ON THE APICAL SIDE OF
 CC NEUROEPITHELIAL CELLS AND OF OTHER EPITHELIA SUCH AS LUNG BUDS,

CC GUT AND URETER BUDS. IN THE ADULT, EXPRESSED AT THE APICAL SIDE
 CC OF THE KIDNEY TUBULES AND OF THE EPENDYMAL LAYER OF THE BRAIN. NOT

CC EXPRESSED IN GUT, LIVER, LUNG, PITUITARY, ADRENAL, HEART OR
 CC SPLEEN.

CC -1- SIMILARITY: BELONGS TO THE PROMININ FAMILY.

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 CC or send an email to license@isb-sib.ch).

CC EMBL; AF039663; AAB86916.1; -

DR EMBL; AF026269; AAB86715.1; -

DR MGD; MGI:1100886; Prom.

KW Signal; Transmembrane; Glycoprotein.

FT SIGNAL 1 19 POTENTIAL.

FT CHAIN 20 867 PROMININ.

FT DOMAIN 108 128 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 129 158 POTENTIAL.

FT DOMAIN 159 179 CYTOPLASMIC (POTENTIAL).

FT TRANSMEM 180 434 EXTRACELLULAR (POTENTIAL).

FT DOMAIN 435 455 POTENTIAL.

FT TRANSMEM 456 487 CYTOPLASMIC (POTENTIAL).

FT DOMAIN 488 508 POTENTIAL.

FT TRANSMEM 509 794 EXTRACELLULAR (POTENTIAL).

FT DOMAIN 795 815 POTENTIAL.

FT TRANSMEM 816 867 CYTOPLASMIC (POTENTIAL).

FT DOMAIN 293 293 POTENTIAL.

FT CARBOHYD 291 291 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 332 332 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 374 374 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 415 415 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 554 554 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 581 581 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 732 732 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 732 732 S -> N (IN REF. 2).

FT CARBOHYD 84 84 K -> N (IN REF. 2).

FT CARBOHYD 94 102 MISSING (IN REF. 2).

FT CARBOHYD 668 668 P -> L (IN REF. 2).

FT CONFLICT 668 668

FT CONFLICT 844 844 G -> D (IN REF. 2).
 SQ SEQUENCE 867 AA; 97112 MW; D442F6372552B3C8 CRC64;
 Query Match 9.0%; Score 86.5; DB 1; Length 867;
 Best Local Similarity 22.7%; Pred. No. 1.9;
 Matches 44; Conservative 30; Mismatches 67; Indels 53; Gaps 10;

QY 18 LHACICQRCSSNTPLTCORCYCNASVTNSVGTNAIWMTCGLSLTSLAVFVLMFL 77
 DB 126 LVGCFRCMRC-----CNK-CGSEMRQKONKPCRRKCLGLVLCILMSGIIY 176
 QY 78 RKISSEPLDEFPNTSGSLGMANIDLEKRTGD-EIIL--PRGLETVVECTCE---- 129
 DB 177 GFVANQOTRIKGTOK-----LAKSNFRDPOTLTLETPEKQIDYVEGYTNTKNA 227
 QY 130 ----DCIKS-----KPKYDSHCFPLPMEGATILVTK-TNDYCKSLPAL-- 172
 DB 228 FSDLDIGVGLGRINDQKPKV-----TPVLEETIKAMATAIKOTKALQWSSSLKS 280

173 ---SATEIKSISA 183
 281 LODAATQMTNLS 294

RESULT 7
 ID FAK2 MOUSE STANDARD; PRT; 1009 AA.
 AC Q90V9;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DE Protein tyrosine kinase 2 beta (EC 2.7.1.112) (Focal adhesion kinase
 2) (FAK2 2) (Proline-rich tyrosine kinase 2) (Cell adhesion kinase
 beta) (CAK beta) (Calcium-dependent tyrosine kinase) (CADTK) (Related
 adhesion focal tyrosine kinase).
 GN PTK2B OR FAK2 OR PYK2 OR RAFPK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=96070905; PubMed=7499242;
 RA Avraham S., London R., Fu Y., Oca S., Hiresowdara D., Li J., Jiang S.,
 RA Pasztor L.M., White R.A., Groopman J.E., Avraham H.;
 RT "Identification and characterization of a novel related adhesion focal
 tyrosine kinase (RAFPK) from megakaryocytes and brain.";
 RT J. Biol. Chem. 270:27742-27751 (1995).
 RN [2]
 RP PHOSPHORYLATION OF TYR-402, AND INTERACTION WITH NEPHROCYSTIN.
 RC MEDLINE=21396557; PubMed=11493697;
 RA Benzing T., Geiske P., Hoepker K., Hildebrandt P., Kim E., Walz G.;
 RT "Nephrocystin interacts with Pyk2, p130(Cas), and tensin and triggers
 phosphorylation of Pyk2.";
 RT Proc. Natl. Acad. Sci. U.S.A. 98:9784-9789 (2001).
 CC -1- FUNCTION: Involved in calcium induced regulation of ion channel
 and activation of the map kinase signaling pathway. May represent
 an important signaling intermediate between neuropeptide activated
 receptors or neurotransmitters that increase calcium flux and the
 downstream signals that regulate neuronal activity. Interacts with
 the SH2 domain of Grb2. May phosphorylate the voltage-gated
 potassium channel protein Kv1.2. Its activation is highly
 correlated with the stimulation of c-Jun N-terminal kinase
 activity (by similarity).
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 tyrosine phosphate.
 CC -1- SUBUNIT: Interacts with Crk-associated substrate (Cas).
 CC -1- NEPHROCYSTIN and GRPase regulator associated with FAK (Graf).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic. Interaction with Nephrocystin
 induces the membrane-association of the kinase.
 CC -1- PTM: Phosphorylated on tyrosines in response to various stimuli
 that elevate the intracellular calcium concentration, as well as

CC by FAK activation. Recruitment by Nephrocystin to cell matrix
 CC adhesions initiates Tyr-402 phosphorylation. In monocytes,
 CC adherence to substrata is required for tyrosine phosphorylation
 CC and kinase activation. Angiotensin II, thapsigargin and L-alpha-
 CC lysophosphatidic acid (LPA) also induce autophosphorylation and
 CC increase kinase activity (by similarity).
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. FAK
 CC SUBFAMILY.
 DR HSP; P08631; IAD5.
 DR MGD; MGI:104908; Ptk2b.
 DR InterPro; IPR000719; Euk_pkinase.
 DR InterPro; IPR005189; Focal AT.
 DR InterPro; IPR001245; Tyr_pkinase.
 DR Pfam; PF00069; pkinase; 1.
 DR Pfam; PF03623; Focal AT; 1.
 DR PRINTS; PR00109; TYRKINASE.
 DR PRODOM; PD000001; Euk_pkinase; 1.
 DR SMART; SM00295; B41; 1.
 DR SMART; SM00219; Tyrc; 1.
 DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE; PS50011; PROTEIN KINASE DOM; 1.
 DR PROSITE; PS00109; PROTEIN KINASE_TYR; 1.
 KW Tyrosine-protein kinase; Transferase; ATP-binding; phosphorylation.
 FT DOMAIN 425 683
 FT NP_BIND 431 439
 FT BINDING 457 457
 FT ACT_SITE 549 549
 FT DOMAIN 701 767
 FT DOMAIN 831 869
 FT DOMAIN 868 1009
 FT MOD_RES 402 402
 FT MOD_RES 579 579
 SQ SEQUENCE 1009 AA; 115821 MW; 963959F560F9605 CRC64;
 Query Match 8.5%; Score 82; DB 1; Length 1009;
 Best Local Similarity 26.9%; Pred. No. 6;
 Matches 29; Conservative 13; Mismatches 34; Indels 32; Gaps 4;

QY 88 EFKNTGSGILGMANIDLEKSR-----TGDEIILPRGLETVVECTCEDCIKSKPKV 138
 DB 249 KFEPT---LAGFANIDQETRYCELIQGNITVDLVIGKIGKIRQLTSQTKPTCLAEFKOI 305

QY 139 DSDHCFPPAME-----EGATILVTKTND-----YCK 166
 DB 306 RSIRCLPHEHQAVVLQIGEGAPQSLXIKTSLAEAWMDLIDGYCR 353

RESULT 8
 ID FAK2 RAT STANDARD; PRT; 1009 AA.
 AC P706D0; O63201; O88489;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DE Protein tyrosine kinase 2 beta (EC 2.7.1.112) (Focal adhesion kinase
 2) (FAK2 2) (Proline-rich tyrosine kinase 2) (Cell adhesion kinase
 beta) (CAK beta) (Calcium-dependent tyrosine kinase) (CADTK).
 GN PTK2B OR FAK2 OR PYK2.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1), AND SEQUENCE OF 310-334; 553-572;
 RP 672-687 AND 989-998.
 RC TISSUE=liver epithelium;
 RX MEDLINE=97094711; PubMed=8939945;
 RA Yu H., Li X., Matchetto G.S., Dy R., Hunter D., Calvo B., Dawson T.L.,
 RA Wilm M., Anderreg R.J., Graves L.M., Bapp H.S.;
 RT "Activation of a novel calcium-dependent protein-tyrosine kinase.
 RT Correlation with c-Jun N-terminal kinase but not mitogen-activated
 RT protein kinase activation.";
 RT J. Biol. Chem. 271:29993-29998 (1996).

[4]
 RN SEQUENCE FROM N.A. (ISOFORM 1).
 RP MEDLINE=96070905; PubMed=7499243;
 RX Avraham S., London R., Fu Y., Oca S., Hiregowdara D., Li J., Jiang S.,
 RA Pasztor L.M., White R.A., Groopman J.E., Avraham H.,
 RT "Identification and characterization of a novel related adhesion focal
 RT tyrosine kinase (RAFTK) from megakaryocytes and brain";
 RL J. Biol. Chem. 270:27742-27751(1995).
 [5]
 RN SEQUENCE FROM N.A. (ISOFORM 2).
 RP TISSUE=Monocytes;
 RX MEDLINE=98211954; PubMed=9545257;
 RA Li X., Hunter D., Morris J., Haekli J.S., Earp H.S.;
 RT "A calcium-dependent tyrosine kinase splice variant in human
 RT monocytes. Activation by a two-stage process involving adherence and a
 RT subsequent intracellular signal";
 RL J. Biol. Chem. 273:9361-9364(1998).
 [6]
 RN SEQUENCE FROM N.A.
 RP Blechschmidt K., Jandrig B., Baumgart C., Dette M.D., Jahn N.,
 RX Menzel U., Schilhabel M.B., Wen G., Taudien S., Rosenthal A.;
 RT Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
 [7]
 RN PHOSPHORYLATION OF TYR-402, MUTAGENESIS OF PRO-859, AND INTERACTION
 RP WITH NEPHROCISTIN.
 RX MEDLINE=21396557; PubMed=11493697;
 RA Benzing T., Gerke P., Hoepker K., Hildebrandt F., Kim E., Walz G.;
 RT "Nephrocystin interacts with Pyk2, p130(Cas), and tensin and triggers
 RT phosphorylation of Pyk2";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:9784-9789(2001).
 [8]
 RN -1- FUNCTION: Involved in calcium induced regulation of ion channel
 CC and activation of the map kinase signaling pathway. May represent
 CC an important signaling intermediate between neuropeptide activated
 CC receptors or neurotransmitters that increase calcium flux and the
 CC downstream signals that regulate neuronal activity. Interacts with
 CC the SH2 domain of Grb2. May phosphorylate the voltage-gated
 CC potassium channel protein Kv1.2. Its activation is highly
 CC correlated with the stimulation of c-Jun N-terminal kinase
 CC activity.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 CC tyrosine phosphate.
 CC -1- SUBUNIT: Interacts with Crk-associated substrate (Cas).
 CC Nephrocystin and Grapase regulator associated with FAK (Graf).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic. Interaction with Nephrocystin
 CC induces the membrane-associated form of the kinase.
 CC -1- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; are
 CC produced by alternative splicing.
 CC -1- TISSUE SPECIFICITY: Most abundant in the brain, with highest
 CC levels in amygdala and hippocampus. Low levels in kidney. Also
 CC expressed in spleen and lymphocytes.
 CC -1- PTM: Phosphorylated on tyrosines in response to various stimuli
 CC that elevate the intracellular calcium concentration, as well as
 CC by PKC activation. Recruitment by Nephrocystin to cell matrix
 CC adhesions initiates Tyr-402 phosphorylation. In monocytes,
 CC adherence to substrate is required for tyrosine phosphorylation
 CC and kinase activation. Angiotensin II, thapsigargin and L-alpha-
 CC lysophosphatidic acid (LPA) also induce autophosphorylation and
 CC increase kinase activity (By similarity).
 CC -1- SIMILARITY: BELONGS TO THE TYR FAMILY OF PROTEIN KINASES. FAK
 CC SUBFAMILY.
 CC -----
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 CC -----
 CC EMBL: U33284; AAC50203.1; -
 CC EMBL: L49207; AAB47217.1; -
 CC EMBL: D45853; BAA08289.1; -
 CC EMBL: U43522; AAC05330.1; -

DR EMBL: S80542; AAB35701.1; -
 DR EMBL: AF311103; -; NOT_ANNOTATED_CDS.
 DR HSSP: P86631; IAD5.
 DR Genew: HGNC:9612; PTK2B.
 DR MIM: 601212; -
 DR InterPro: IPR000719; Euk_pkinase.
 DR InterPro: IPR005189; Focal_AT.
 DR InterPro: IPR001245; Tyr_pkinase.
 DR Pfam: PF00069; pkinase; 1.
 DR Pfam: PF01623; Focal_AT; 1.
 DR ProDom: PD000001; Euk_pkinase; 1.
 DR SMART: SM00295; B41; 1.
 DR SMART: SM00219; TykC; 1.
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE: PS00109; PROTEIN_KINASE_TYR; 1.
 DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
 KM Tyrosine-protein kinase; Transferase; ATP-binding; Phosphorylation;
 KW Alternative splicing.
 FT DOMAIN 425 683
 FT NP_BIND 431 439
 FT BINDING 457 457
 FT ACT_SITE 549 549
 FT DOMAIN 702 767
 FT DOMAIN 831 869
 FT DOMAIN 868 1009
 FT MOD_RES 402 402
 FT MOD_RES 579 579
 FT VAR_SEQ 739 780
 FT MUTAGEN 859 859
 FT CONFLICT 23 23
 FT CONFLICT 256 256
 FT CONFLICT 435 435
 FT CONFLICT 780 780
 SQ SEQUENCE 1009 AA; 115874 MW; 420B21046274E7C2 CRC64;
 Query Match 8.2%; Score 79.5; DB 1; Length 1009;
 Best Local Similarity 32.1%; Pred. No. 10;
 Matches 25; Conservative 9; Mismatches 29; Indels 15; Gaps 3;
 QY 88 EFKATGSGGLGMANIDLEKSR-----TGDILLRGLGYTYVECTCEDCIKSKRV 138
 DB 249 KEFNT---LAGPANIIDQTYRELLIGMNITVDVIGKGIROLTSQAKPTGLAEFKOI 305
 QY 139 DSDHCPFLPAMEGATIL 156
 DB 306 RIRICLPL---REGQAVL 320
 RESULT 10
 ID T13X HUMAN STANDARD; PRT; 293 AA.
 AC 014836;
 DT 15-JUN-2002 (rel. 41, Created)
 DT 15-JUN-2002 (rel. 41, Last sequence update)
 DT 15-JUN-2002 (rel. 41, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 13B (Transmembrane
 DE activator and CAML interactor).
 GN TNFRSF13B OR TACT.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_Taxid:9606;
 RP [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=B-cell;
 RX MEDLINE=97458245; PubMed=9311921;
 RA von Buelow G.-U., Biam R.J.;
 RT "NF-AT activation induced by a CAML-interacting member of the tumor
 RT necrosis factor receptor superfamily";
 RL Science 278:138-141(1997).
 RN [2]
 RP SEQUENCE FROM N.A.

CC TISSUE=Blood;
 RA Strausberg R.;
 RN Submitted (Apr-2002) to the EMBL/Genbank/DBJ databases.
 [3]
 RP FUNCTION.
 RX MEDLINE=20519647; PubMed=10956646;
 RA Gan Y., Bressette D., Carrell J.A., Kaufman T., Peng P., Taylor K.,
 RA Gan Y., Cho Y.H., Garcia A.D., Gollatz E., Dimke D., Lafleur D.,
 RA Milgrom S., Nardelli B., Wei P., Ruben S.M., Ullrich S.J.,
 RA Olsen H.S., Kanakara P., Moore P.A., Baker K.P.;
 RT "Tumor necrosis factor (TNF) receptor superfamily member TNFRI is a
 high affinity receptor for TNF family members APRIL and BLYS.";
 RL J. Biol. Chem. 275:35478-35485(2000).
 RN FUNCTION.
 RP MEDLINE=21170294; PubMed=10973284;
 RA Yu G., Boone T., Delaney J., Hawkins N., Kelley M., Ramakrishnan M.,
 RA McCabe S., Qiu W.R., Kornuc M., Xia X.-Z., Guo J., Stollin M.,
 RA Boyle W.J., Sarosi I., Hsu H., Senaldi G., Theill L.E.;
 RA "APRIL and TNF-1 and receptors BCMA and TNFR1: system for regulating
 humoral immunity.";
 CC Nat. Immunol. 1:252-256(2000).
 CC -1- FUNCTION: Receptor for TNFSF13/APRIL and TNFSF13B/TALL1/BAFF/BLYS
 that binds both ligands with similar high affinity. Mediates
 calcineurin-dependent activation of NF-kappa-B, as well as activation
 of NF-kappa-B and AP-1. Involved in the stimulation of B- and T-
 cell function and the regulation of humoral immunity.
 CC -1- SUBUNIT: Binds TRAF2, TRAF3 and TRAF6. Binds the NH2-terminal
 domain of CARD11 with its C-terminus.
 CC -1- SUBCELLULAR LOCATION: Type III membrane protein.
 CC -1- TISSUE SPECIFICITY: Highly expressed in spleen, thymus, small
 intestine and peripheral blood leukocytes. Expressed in resting B-
 cells and activated T-cells, but not in resting T-cells.
 CC -1- SIMILARITY: CONTAINS 2 TNFR-CYS REPEATS.
 CC -1- CAUTION: It is uncertain whether Met-1 or Met-31 is the initiator.
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 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: AF023614; AAC51790.1; -
 DR EMBL: BC028072; AAH28072.1; -
 DR Genew, HGNC:18153; TNFRSF13B.
 CC MIM: 604907; -
 DR InterPro: IPR001368; TNFR_C6.
 DR PROSITE: PS00652; TNFR_NGFR_1; 1.
 DR PROSITE: PS00650; TNFR_NGFR_2; FALSE NEG.
 KW Receptor; Immune response; Signal-anchor; Transmembrane; Glycoprotein;
 KW Repeat.
 FT DOMAIN 1 165
 FT TRANSMEM 166 186
 FT FT
 FT FT
 FT DOMAIN 1 165
 FT TRANSMEM 166 186
 FT FT
 FT FT
 FT REPEAT 70 104
 FT DISULFID 34 47
 FT DISULFID 50 62
 FT DISULFID 54 66
 FT DISULFID 71 86
 FT DISULFID 89 100
 FT DISULFID 93 104
 FT CAROHD 128 128
 FT CONFLICT 251 251
 FT SEQUENCE 293 AA; 31816 MW; 411799F3DE17A5EB CRC64;
 Query Match 8.1%; Score 78.5; DB 1; Length 293;
 Best Local Similarity 19.9%; Pred. No. 3.4; 73; Indels 57; Gaps 10;
 Matches 41; Conservative 35; Mismatches 73; Indels 57; Gaps 10;

QY 8 CSQNEFDSLLHACIPQGRCSSTNPPLTGRCYCNASVTSVKGT--NALIMTCLGLSLI 65
 Db 34 CPBEGYMDPLIGTMCSCRTICNHQS--QRTCAFCRSLSCRKQGFYDHLRLDSCASII 92
 QY 66 I-----SLAVFVMTL-----LRKISEPLKDEKRTGSGLLGANIDLES----- 107
 Db 93 CGQHPKQCAVCENKLRSPVNLPELRLRQSGEVENNSDNGR-YQGLEHSGSEASPALP 151
 QY 108 ---RTGDEILIPRG-----LEYVEBCTCEDCIKSKP-----KYD 139
 Db 152 GIKSADQVALYVSTGLCLCAVLCFLVYAVACFLKRGDPCSCP--RSRPRGSPAKSS 209
 QY 140 SDHCPPLPMEGATILVTTKNDYC 165
 Db 210 QDH-----AMEAGSPVSTSPPEVETC 230
 RESULT 11
 ID YD57 METVA STANDARD; PRT; 343 AA.
 AC 058752;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DB Putative potassium channel protein M01357.
 GN M01357.
 OS Methanococcus jannaschii.
 OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
 OC Methanocaldococcaceae; Methanocaldococcus.
 OK NCBI_TaxID=2190;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
 RX MEDLINE=96317999; PubMed=8688087;
 RA Bult C.J., White O., Olsen G.V., Zhou L., Fleischmann R.D.,
 RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
 RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
 RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
 RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhmann J.L., Nguyen D.,
 RA Uterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hama M.C.,
 RA Cotton M.D., Roberts K.M., Hirst M.A., Kaine B.P., Borodovsky M.,
 RA Klenk H.-P., Frazer C.M., Smith H.O., Weese C.R., Venter J.C.;
 RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
 jannaschii.";
 RL Science 273:1058-1073(1996).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -1- SIMILARITY: STRONG, TO M.JANNASCHII M0138.1.
 CC -1- SIMILARITY: TO EUKARYOTIC POTASSIUM CHANNELS.
 CC -----
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 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: U67575; AAB99365.1; -
 DR HSSP: Q54397; IBL8.
 DR TIGR: M01357; -
 DR InterPro: IPR001622; K+channel pore.
 DR InterPro: IPR000309; TrKA Kupfke.
 DR InterPro: IPR003148; TrKA_N.
 DR Pfam: PF02080; TrKA-C; 1.
 DR Pfam: PF02254; TrKA-N; 1.
 KW Hypothetical protein; Transmembrane; Transport; Ion transport;
 KW Ionic channel; Complete proteome.
 FT TRANSMEM 8 28
 FT TRANSMEM 30 50
 FT TRANSMEM 62 82
 FT SEQUENCE 343 AA; 38863 MW; 61231B0C001B54C4 CRC64;
 Query Match 8.1%; Score 78.5; DB 1; Length 343;

Oy		Best Local Similarity	20.4%	Pred. No. 4:	
Db		Matches	39;	Conservative	35; Mismatches 66; Indels 51; Gaps 8
Oy	12 EYFDSLHACIPQCLRCSNTPPLTCQRYCNASVTSNKGINAIIAMTCLGSLITSIAVF	71	:	:	:
Db	32 DYFTLALYSVI-----TIITTGCDPTPTFLRLTVLLCGVGIVWMLPSL	80	:	:	:
Oy	72 VLMFL-----LRKISS--EPLKDFFKNYSGSGLGMA-----NIDLEKSRTGD	111	:	:	:
Db	81 IAEFLVEEGKEEFPAVLKKMKIKTKLKOHYIICGGRLOKVNGEKFIENIIFAIADINE	140	:	:	:
Oy	112 EII-----LPREGLEYVEECTCEDCISKPXY-----DSDHCF-PLPAMEBG	152	:	:	:
Db	141 DVLKEERYEPDKPFYIVGDAKKEHVLC-KAKIDRAKGIATLPEDADVFLTAREIN	199	:	:	:
Oy	153 ATLIWTKTND	163	:	:	:
Db	200 PHLITATADE	210	:	:	:
JLT 12					
ID	TJIX MOUSE	STANDARD;	PRT;	249 AA.	
AC	Q9ERT35; Q9DBZ3;				
DT	15-JUN-2002 (Rel. 41, Created)				
DT	15-JUN-2002 (Rel. 41, Last sequence update)				
DT	15-JUN-2002 (Rel. 41, Last annotation update)				
DE	Tumor necrosis factor receptor superfamily member 13B (Transmembrane activator and CAML interactor).				
DE	TMPSRF13B OR TACT1.				
OS	Mus musculus (Mouse).				
OC	Eumetazoa; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX	NCBI_TaxId=10090;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	Tissue=Spleen;				
RX	MEDLINE=21177254; PubMed=10881172;				
RA	van M., Marsters S.A., Grewal I.S., Wang H., Ashkenazi A., Dixit V.M.;				
RT	"Identification of a receptor for Bly's demonstrates a crucial role in humoral immunity."				
RL	Nat. Immunol. 1:37-41 (2000).				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=C57BL/6J; TISSUE=Lung;				
RX	MEDLINE=C57BL/6J; PubMed=11217851;				
RA	Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I., Salto T., Okazaki Y., Gotjoberi T., Bono H., Kasukawa T., Saico R., Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Fletschmann W., Gaasterland T., Glasi C., King B., Kochiya H., Kusel P., Lewis S., Matsumoto Y., Nikolaev I., Pesole G., Quackenbush J., Schmitt L.M., Stambli F., Suzuki R., Tomita M., Wagner L., Washio T., Sakai K., Okido T., Furuno M., Anjo H., Baladrelli R., Barsh G., Blake J., Bonfelli D., Bojunga N., Carninci P., de Bonaldo M.F., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Gruenich S., Hill D., Hofman M., Huie D.A., Kamuya M., Lee N.H., Lyons P., Marchionni L., Mashima J., Mazzarelli U., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shihata Y., Storch K.-F., Suzuki H., Toyooka K., Wang K.H., Weltz C., Whitaker C., Wilming L., Wysshne-Boris A., Yoshida K., Haegawa Y., Kawaji H., Kohlsuki S., Hayashizaki Y.;				
RT	"Functional annotation of a full-length mouse cDNA collection";				
RL	Nature 409:685-690 (2001).				
RP	FUNCTION.				
RX	MEDLINE=20341628; PubMed=10880535;				
RA	Xia X.-Z., Treanor J., Senaldi G., Khare S.D., Boone T., Kelley M., Thell L.E., Colombiero A., Solovyev I., Lee P., McCabe S., Elliott R., Miller K., Hawkins N., Guo J., Stolinska M., Yu G., Wang J., Delaney J.,				

R	Meng S.Y., Boyle M.J., Hsu H.;
RA	"TRAC1 is a TRAF-interacting receptor for TLR1-1, a tumor necrosis
RT	factor family member involved in B cell regulation.";
RL	J. Exp. Med. 192:137-143(2000).
RN	[4]
RP	FUNCTION.
RX	MEDLINE=21322748; PubMed=11429548;
RY	Wang H., Marsters S.A., Baker T., Chan B., Lee W.P., Fu L., Tunas D.,
SA	Yang M., Dixit V.M., Ashkenazi A., Grewal I.S.;
RT	"TRAC1-ligand interactions are required for T cell activation and
RL	collagen-induced arthritis in mice."
CC	Nat. Immunol. 2:632-637(2001).
CC	-1- FUNCTION: Receptor for TNFSF13/APRIL and TNFSF1B/TALL1/BALF/BLYS
CC	that binds both ligands with similar high affinity. Mediates
CC	calcineurin-dependent activation of NF-kappa-B, as well as activation
CC	of NF-kappa-B and AP-1. Involved in the stimulation of B- and T-
CC	cell function and the regulation of humoral immunity (By
CC	similarity).
CC	-1- SUBUNIT: Binds TRAF2, TRAF5 and TRAF6. Binds the NH2-terminal
CC	domain of CMTLG with its C-terminus (By similarity).
CC	-1- SUBCELLULAR LOCATION: Type III membrane protein (Probable).
CC	-1- SIMILARITY: CONTAINS 2 TNFR-CVS REPEATS.
CC	-----
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CC	or send an email to licenses@sib-sib.ch).
CC	-----
DR	EMBL; AF257673; AACG0081.1; -
DR	EMBL; AK004668; BAB23457.1; -
DR	MGI; MG11889411; Trnfrsfl3b.
DR	PROSITE; PS00652; TNFR_NGFR_1; 1.
DR	PROSITE; PS00650; TNFR_NGFR_2; 2.
KM	Receptor; Immune response; Signal-anchor; Transmembrane; Repeat.
FT	DOMAIN
FT	TRANSEM
FT	129 149
FT	SIGNAL-ANCHOR (TYPE III MEMBRANE PROTEIN)
FT	(POTENTIAL).
FT	CYTOPLASMIC (POTENTIAL).
FT	REPEAT
FT	5 249
FT	38
FT	TNFR-CVS 1.
FT	REPEAT
FT	42 76
FT	19
FT	TNFR-CVS 2.
FT	DISULFD
FT	6 19
FT	BY SIMILARITY.
FT	DISULFD
FT	22 24
FT	BY SIMILARITY.
FT	DISULFD
FT	26 34
FT	BY SIMILARITY.
FT	DISULFD
FT	43 58
FT	BY SIMILARITY.
FT	DISULFD
FT	61 72
FT	BY SIMILARITY.
FT	DISULFD
FT	65 76
FT	BY SIMILARITY.
FT	CONFLICT
FT	137 137
FT	I-> F (IN REF. 2).
FT	SEQUENCE
FT	249 AA; 26947 MW; CBFAFD61C2931D81 CRC64;
Q	Query Match
B	Best Local Similarity 8.0%; Score 77; DB 1; Length 249;
M	Matches 43; Conservative 21; Mismatches 70; Indels 64; Gaps 11
O	10 QNEFPDSLHACTPCQLRCSSNTPTLTQRVCN--ASVTN-----SYKGTN 53
D	47 QGRYYDHLLGACVSCDSCTGDH--POCAHCEKRPRSQANVLPELGPAGEVEVERSN 104
O	54 A-----ILMTCLGLSLIISLAIVFL--MFLRKISSEPLKDEPFKN 91
D	105 SGRIQGSHHGGLRLSSDQLTYCTLGVCLCAIRCFEVALAFLRR--GEPLSQPRAG 162
O	92 TGSGILGNANTIDLEKSRTGBIIL--PGLEYVEECTCEDCI-----KSKPVDSH 142
D	163 PRGSQANSFHARRPVTACEDEVATSPQVE-----TCSFCPPERSSPTQESAPRSLSGIH 216
O	143 CF-----PLPMEGATTI 155
D	217 GFAGTAAPQPCCR--ATV 232

RESULT 13

YCSB_SCHPO	ID	YCSB_SCHPO	STANDARD:	PRT:	638 AA.
AC	074910				
DT	16-OCT-2001	(Rel. 40, Created)			
DT	16-OCT-2001	(Rel. 40, Last sequence update)			
DT	15-JUN-2002	(Rel. 41, Last annotation update)			
DE	Hypothetical WD-repeat protein C613.12c in chromosome III.				
CN	SPCC613.12C				
OS	Schizosaccharomyces pombe (Fission yeast).				
OC	Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;				
OC	Schizosaccharomycetales; Schizosaccharomycetaceae;				
OC	Schizosaccharomyces.				
NCBI_TaxID=4896;					
[1]					
RP	SEQUENCE FROM N.A.				
RC	STRAIN=972;				
RX	MEDLINE=21849401; PubMed=11859360;				
W	Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,				
W	Brooke J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,				
W	Sgroves K., Brown D., Brown S., Chillingworth T., Churcher C.M.,				
W	Collins M., Connor R., Cronin A., Davis P., Fellwell T., Fraser A.,				
W	Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,				
W	Holroyd S., Hornby T., Howarth S., Huckle E.J., Hunt S., Jørgels K.,				
W	James K., Jones B., Jones M., Leacher S., McDonald S., McLean V.,				
W	Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,				
W	Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitch E.,				
W	Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,				
W	Skellton J., Simmonds S., Squares R., Squares S., Stevens K.,				
W	Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,				
W	Woodward J., Volkhardt G., Aert R., Robben J., Grymoprez B.,				
W	Welters I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,				
W	Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,				
W	Bozzym K., Langer I., Beck A., Lehnach H., Reinhardt R., Pohl T.M.,				
W	Eger P., Zimmermann W., Wedler H., Wambutt R., Punnett B.,				
W	Goffeau A., Cadiau E., Dreano S., Gloux S., Leleau V., Motier S.,				
W	Gallbert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,				
W	Lucas M., Rochet M., Gallierdin C., Tallada V.A., Garzon A., Rhode G.,				
W	Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,				
W	Domínguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,				
W	Cerutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,				
W	Shpakovski G.V., Ussery D., Barrett B.G., Nurse P.;				
W	"The genome sequence of Schizosaccharomyces pombe.";				
W	Nature 415:871-880(2002).				
W	-I- SIMILARITY: CONTAINS 4 WD REPEATS (TRP-ASP DOMAINS).				
W					
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W	or send an email to license@isb-stb.ch .				
W					
W	EMBL; AL031644; CAA21064.1; -				
W	InterPro; IPR001680; WD40.				
W	Pfam; PF00400; WD40.				
W	PRINTS; PR00320; GPROTINERPT.				
W	SMART; SMO0320; WD40; 4				
W	PROSITE; PS00678; WD_REPEATS_1; 2				
W	PROSITE; PS00682; WD_REPEATS_2; 2				
W	PROSITE; PS50294; WD_REPEATS_REGION; 1				
W	Hypothetical protein; Repeat; WD repeat.				
W	REPEAT 297 336				
W	REPEAT 486 525				
W	REPEAT 544 583				
W	REPEAT 587 626				
W	SEQUENCE 638 AA; 71536 MW; 6CD360D8748AA98 CRC64;				

```

OY 12 EYFSLHACIPCOLRQSSNPTLTQRCYCNASTVYKGNALIMTCLSLITSLAVF 71
Dd 42 EIVPFRABEPCP-----KPSLISHSIAKPSNNKR-----LEIQLMISTGF 88
OY 72 VLMFLRKISSEPKDFKFTKGSGLGMANIDLEKRTGDEIILPRGLETVEEC----- 126
Dd 89 L-----PNSRPLTSERVKRGHTL-----LSNSTIGDQKPSLHVDFPEECFIQE 134
OY 127 -----TCEDCIKSPKVDSDHCFPLPAMEEGATIVT 158
Dd 135 AKLKFQPNVSQVFNDAVSTHISPLPGRAVEDC-----QKEIFIDNPSLSFVDKHAIIIRT 190
OY 159 TKTN-----DYCKS 167
Dd 191 YKKNKKLLPDYLSK 204

RESULT 14
SRK6_BRAOL
ID_SRK6_BRAOL STANDARD; PRT; 849 AA.
AC Q09092;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Putative serine/threonine kinase receptor precursor (EC 2.7.1.37)
DE (S-receptor kinase) (SRK).
GN SRK6.
OS Brassica oleracea (Cauliflower).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophytes; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eustosids II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=3712;
[1]
RN RP SEQUENCE FROM N.A.
RC STRAIN=cv. S6S6; TISSUE=Stigma;
RC MEDLINE=92020942; PubMed=1681543;
RA Stein J.C., Howlett B., Boyes D.C., Nasrallah M.E.;
RT "Molecular cloning of a putative receptor protein kinase gene encoded
RT at the self-incompatibility locus of Brassica oleracea."
RL Proc. Natl. Acad. Sci. U.S.A. 88:8816-8820(1991).
CC -1- FUNCTION: INVOLVED IN SPOROPHYTIC SELF-INCOMPATIBILITY SYSTEM
CC (THE INABILITY OF FLOWERING PLANTS TO ACHIEVE SELF-
CC FERTILIZATION), PROBABLY ACTING IN COMBINATION WITH S-LOCUS-
CC SPECIFIC GLYCOPROTEINS. INTERACTION WITH A LIGAND IN THE
CC EXTRACELLULAR DOMAIN TRIGGERS THE PROTEIN KINASE ACTIVITY OF THE
CC CYTOPLASMIC DOMAIN.
CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -1- SUBCELLULAR LOCATION: Type 1 membrane protein.
CC -1- TISSUE SPECIFICITY: PREDOMINANTLY IN THE PISTIL AND ANTHER.
CC -1- POLYMORPHISM: THERE ARE A NUMBER OF DIFFERENT S ALLELES IN
CC B. OLERACEA, POSSIBLY PROVIDING THE RECOGNITION SPECIFICITY.
CC -1- SIMILARITY: THE EXTRACELLULAR DOMAIN IS SIMILAR TO S-LOCUS
CC GLYCOPROTEINS OF BRASSICA, WHILE THE INTRACELLULAR DOMAIN IS
CC A SER/THR-PROTEIN KINASE RELATED TO RAF KINASES.
CC -----
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CC -----
CC EMBL; M76647; AAA33000.1; ALT TERM.
DR InterPro; IPR001480; B_lectin.
DR InterPro; IPR000719; Euk_kinase.
DR InterPro; IPR003609; Pan_app.
DR InterPro; IPR004040; GRY_kinase.
DR InterPro; IPR002290; Ser_thr_kinase.
DR InterPro; IPR000858; Slocus_glycop.
DR Pfam; PF00069; pkinase; 1.
DR Pfam; PF00954; S_locus_glycop; 1.
DR Pfam; PF01453; Agglutinin; 1.
DR

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